

Shotgun Metagenomics

ComBEE 'Omics Study Group Discussion Session

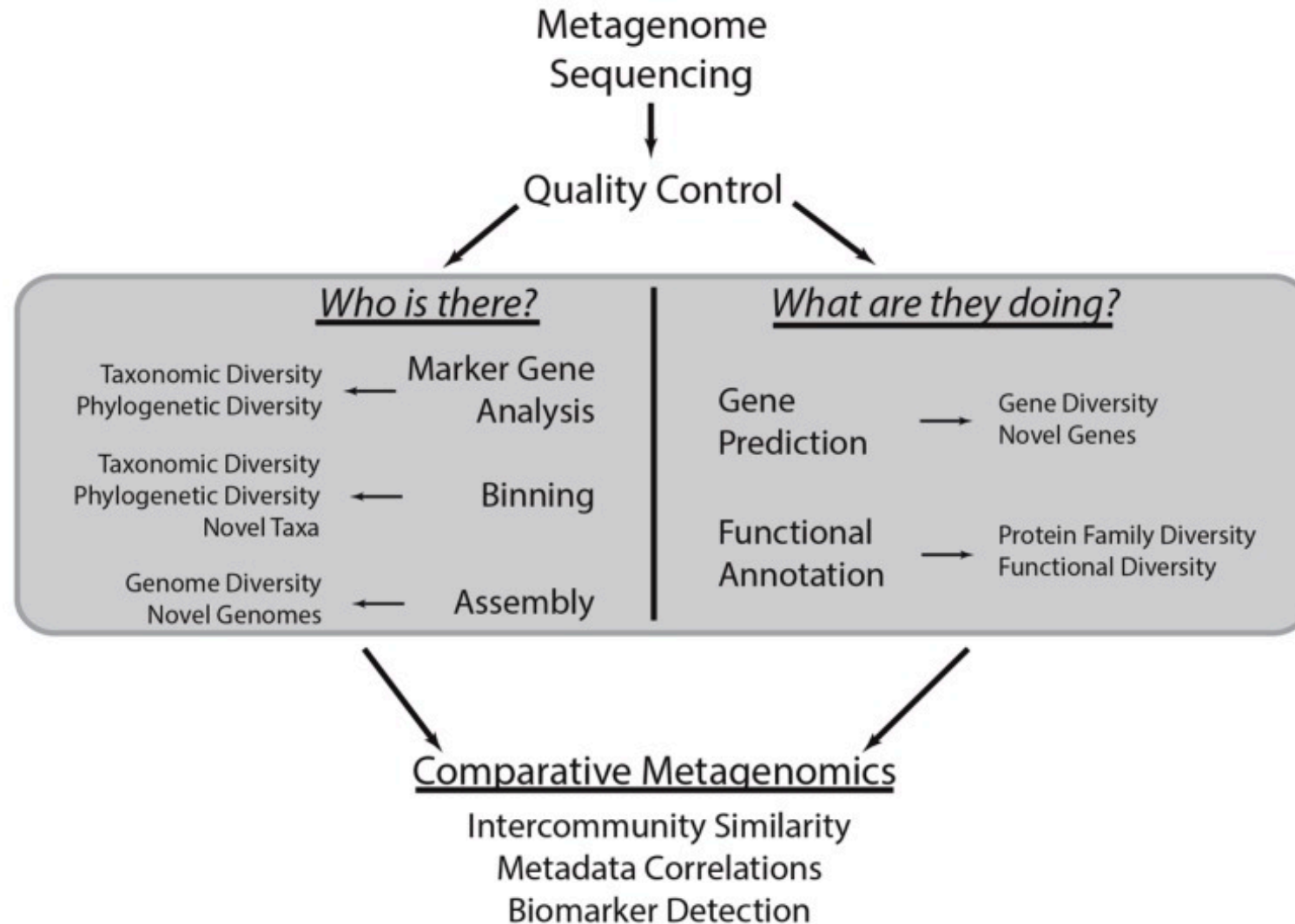
2019-10-24

Notes: <https://bit.ly/2JhRYjx>

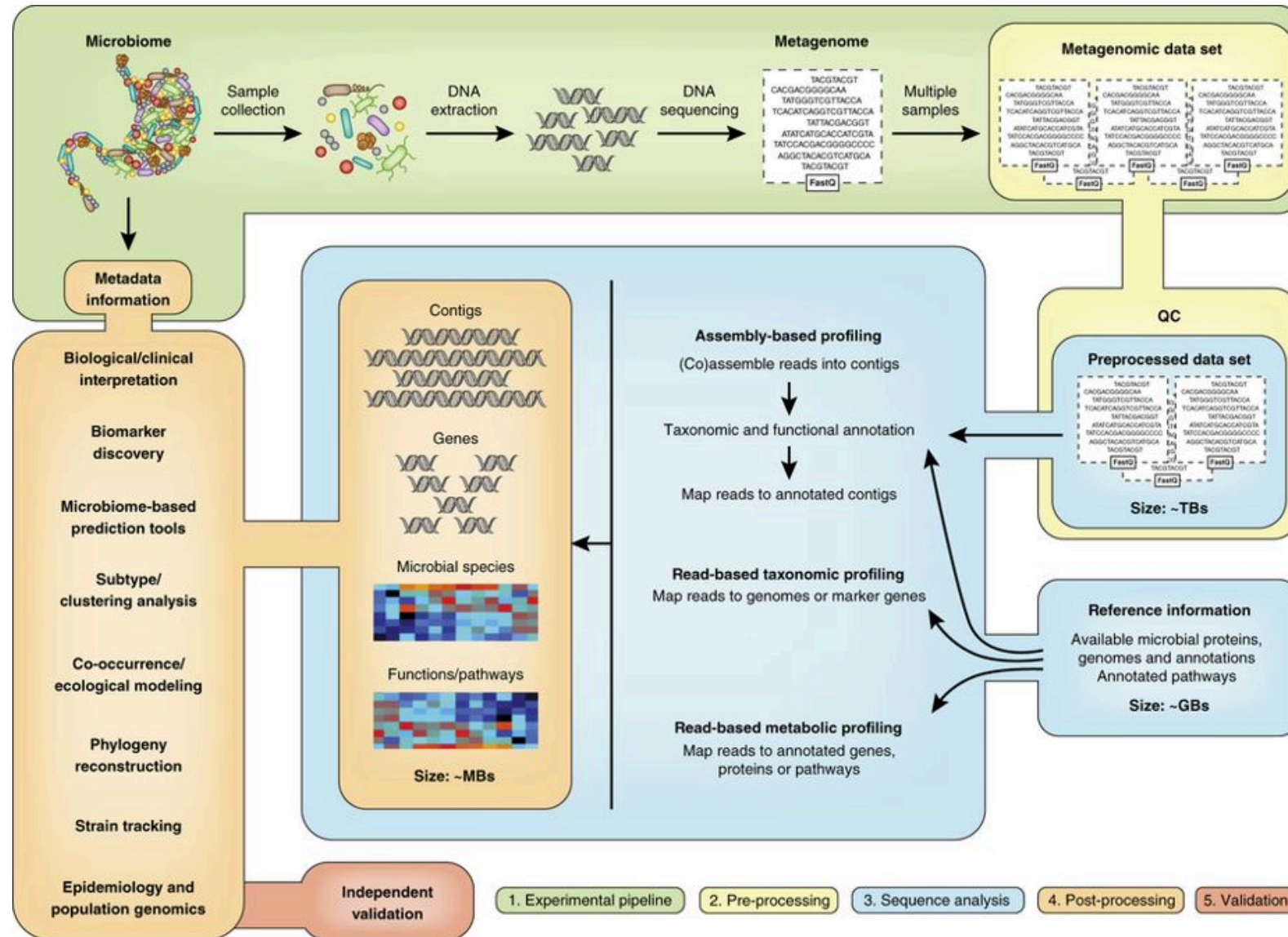
Introductions

1. Name
2. Position
3. Department/Affiliation
4. Area of Research

Shotgun Metagenomics



Shotgun Metagenomics



General Workflow Steps

1. Quality filter reads
2. Assemble into longer contigs
3. Map to a reference database
4. Classify taxonomical composition
5. Assign gene functions
6. Compare enriched species/functions between groups of interest

Discussion

1. What are your research questions?
2. Why are you interested in applying shotgun metagenomics to your research?
3. Have you used 16S amplicon sequencing in your research? What do you want to address in your research that 16S can't answer?
4. What are the analytical barriers for applying shotgun metagenomics to your research?
5. What are the essential tools you need to learn to apply shotgun metagenomics to your research?